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OM nucleic - nucleic search, using sw model

Run on: June 1, 2003, 15:24:09 ; Search time 120.319 Seconds
(without alignments)
5689.057 Million cell updates/sec

Title: US-09-625-573-1

Perfect score: 2232
Sequence: 1 GGATGGAACAGGACGACATT.....TATAACTATGTTGATAAAAG 2232

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA.*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2232	100.0	2232	1	US-08-450-393A-1
2	2232	100.0	2232	3	US-08-446-669-1
3	2232	100.0	2232	5	PCT-US95-00476-1
4	980	43.9	1979	1	US-08-450-393A-3
5	980	43.9	1979	3	US-08-446-669-3
6	980	43.9	1979	5	PCT-US95-00476-3
7	635.6	28.3	1059	4	US-09-517-605-8
8	632.6	28.3	1059	4	US-08-724-984A-3
9	632.6	28.3	1071	3	US-09-087-232A-14
10	632.6	28.3	1376	3	US-09-087-232A-12
11	632.6	28.3	1477	4	US-08-833-752-2
12	632.6	28.3	3383	4	US-08-861-105-13
13	632.6	28.3	3383	4	US-08-575-967A-1
14	629.4	28.2	5674	4	US-09-293-170-3
15	629.4	28.2	1414	3	US-08-466-343D-1
16	612.6	27.4	1344	3	US-09-087-232A-16
17	612.6	27.4	1442	4	US-08-833-752-3
18	588.2	26.4	2440	4	US-08-724-984A-1
19	376	16.8	792	4	US-08-833-752-1
20	325	14.6	2156	1	US-08-012-988A-1
21	323.4	14.5	1065	4	US-08-847-296B-2
22	323.4	14.5	1915	4	US-08-575-967A-3
23	308.6	13.8	461	3	US-09-087-232A-11
24	288.4	12.9	1607	3	US-08-875-573-19
25	288.4	12.9	1695	4	US-09-232-878-1
26	264	11.8	1161	1	US-08-153-848-31
27	264	11.8	1161	5	PCT-US93-11153-31

28 264 11.8 2254 1 US-08-153-848-27 Sequence 27, Appl
29 264 11.8 2254 3 US-09-293-843A-27 Sequence 27, Appl
30 264 11.8 2254 4 US-09-088-337B-27 Sequence 27, Appl
31 264 11.8 2254 5 PCT-US93-11153-27 Sequence 31, Appl
32 264 11.8 3119 3 US-09-293-843A-31 Sequence 31, Appl
33 264 11.8 3119 4 US-09-088-337B-31 Sequence 1, Appl
34 250.4 11.2 1586 1 US-08-461-244-1 Sequence 1, Appl
35 176 7.9 1050 4 US-08-681-192-1 Sequence 1, Appl
36 175.6 7.9 1200 5 PCT-US95-03032-1 Sequence 4, Appl
37 172.8 7.7 1664 4 US-09-045-583-4 Sequence 4, Appl
38 172.8 7.7 1664 4 US-09-534-185-4 Sequence 6, Appl
39 171.8 7.7 1137 4 US-09-045-583-6 Sequence 6, Appl
40 171.8 7.7 1137 4 US-09-534-185-6 Sequence 1, Appl
41 167.6 7.5 1200 5 PCT-US92-02977-1 Sequence 1, Appl
42 160 7.2 2577 4 US-09-266-464-1 Sequence 65, Appl
43 155.2 7.0 2085 3 US-09-299-843A-65 Sequence 65, Appl
44 155.2 7.0 2085 4 US-09-088-337B-65 Sequence 5, Appl
45 151.4 6.8 1106 5 PCT-US92-02977-5 Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-08-450-393A-1
; Sequence 1, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,393A
; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816COOLEYPA
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2232 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 40..1161
; US-08-450-393A-1

Query Match 100.0%; Score 2232; DB 1; Length 2232;
Best Local Similarity 100.0%; Pred. No. 0;

[illegible]

RESULT 3

RESULT 3
PCT-US95-00476-1

201 0355 00470-1
; Sequence 1, Application PC/TUS9500476

GENERAL INFORMATION:

APPLICANT: The Regents of the University of California

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Qy	1561	AGGAGTTGGAAAGTGTGTGATCTGTGGGCACANTAGCCTATGTGCGATCGCAGCAICTAAGTA	1620
Db	1561	AGGAGTTGGAAAGTGTGTGATCTGTGGGCACANTAGCCTATGTGCGATCGCAGCATCTAAGTA	1620
Qy	1621	ATGATGTCGTTTGAATCACAGATACGCTCCATCGCTGTCTATCCTACGCTGGATCTCCATT	1680
Db	1621	ATGATGTCGTTTGAATCACAGATACGCTCCATCGCTGTCTATCCTACGCTGGATCTCCATT	1680
Qy	1681	CTCTCAGGCTTGCTGCCAAAAGCCCTTTGTGTTTGTGTTTGTATCATATGAAGTCATGC	1740
Db	1681	CTCTCAGGCTTGCTGCCAAAAGCCCTTTGTGTTTGTGTTTGTATCATATGAAGTCATGC	1740
Qy	1741	GTTTAAATCACANTCGAGTGTTTTCAGTGCTGCGAGATGCTCTTGATGCTCATATGTGTCC	1800
Db	1741	GTTTAAATCACANTCGAGTGTTTTCAGTGCTGCGAGATGCTCTTGATGCTCATATGTGTTC	1800
Qy	1801	CTAATTTCGCCAGTGGGAACCTCTAAATCAAAATTTGGCTTCTAATCAAAGCTTTTAAACCCCT	1860
Db	1801	CTAATTTCGCCAGTGGGAACCTCTAANTCAAATTTGGCTTCTAATCAAAGCTTTTAAACCCCT	1860
Qy	1861	ATTGTTAAAGAATGGAAGGTGGAGAAGCTCCCTGAAAGTAAGCAAGACTTTCCCTCTTAGT	1920
Db	1861	ATTGTTAAAGAATGGAAGGTGGAGAAGCTCCCTGAAAGTAAGCAAGACTTTCCCTCTTAGT	1920
Qy	1921	CGAGCCAAGTTAAGAATGTTCTTATGTTGCCAGTGTGTTTCTGATCTGATGCAAGCAAG	1980
Db	1921	CGAGCCAAGTTAAGAATGTTCTTATGTTGCCAGTGTGTTTCTGATCTGATGCAAGCAAG	1980
Qy	1981	AAACACTGGGCTTCTAGAACCAAGCAACTTGGGAACCTAGACTCCCAAGCTGGACTATGSC	2040
Db	1981	AAACACTGGGCTTCTAGAACCAAGCAACTTGGGAACCTAGACTCCCAAGCTGGACTATGSC	2040
Qy	2041	TCTACTTTTCAGGCCACATGGCTTAAAGAAGGTTTCAGAAAGAAGTGGGGACAGAGCAGAAC	2100
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Qy	2101	TTTTCACCTTCATATATTTGATATCATCTTAATGAATGCATAAAATGTTAAGTTGATGGTGA	2160
Db	2101	TTTTCACCTTCATATATTTGATATCATCTTAATGAATGCATAAAATGTTAAGTTGATGGTGA	2160
Qy	2161	TGAATGTAAATACTCTTTTAAACAACTATGATTTTGGAAAAATAAATCAATGCTATAACTA	2220
Db	2161	TGAATGTAAATACTCTTTTAAACAACTATGATTTTGGAAAAATAAATCAATGCTATAACTA	2220
Qy	2221	TGTTGATAAAAG	2232
Db	2221	TGTTGATAAAAG	2232

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RECORD 4
US-08-450-393A-3
; Sequence 3, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,393A
FILING DATE: May 25, 1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: UCAL-237/020S
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5165
TELEFAX: 415-8857-0663
TELEX: 380816CooLeypA
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1979 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 81..1160
US-08-450-393A-3

Query Match 43.9%; Score 980; DB 1; Length 1979;
Best Local Similarity 100.0%; Pred. No. 2.3e-270;

Matches 980; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GGATTGAACAAGGACGCAATTCCTCCAGTACATCCACAAAGTGTCACATCTCGTCT 60
DB 42 GGATTGAACAAGGACGCAATTCCTCCAGTACATCCACAAAGTGTCACATCTCGTCT 101
QY 61 CGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAGTCCACACCTTTTGGATTATGAT 120
DB 102 CGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAGTCCACACCTTTTGGATTATGAT 161
QY 121 TACGGTGTCTCCCTGTATCAATTTGACGTGAAGCAAAATGGGGGCCCAACTCTGCCTCCG 180
DB 162 TACGGTGTCTCCCTGTATCAATTTGACGTGAAGCAAAATGGGGGCCCAACTCTGCCTCCG 221
QY 181 CTCTACTCGTGTCTTCACTCTTTGGTTTGGGCAACATCGTGTCTCTCATCTTA 240
DB 222 CTCTACTCGTGTCTTCACTCTTTGGTTTGGGCAACATCGTGTCTCTCATCTTA 281
QY 241 ATAACTGCAAAAGCTGAAGTGTGACTGACATTTACCTGCTCAACCTGGCCATCTCT 300
DB 282 ATAACTGCAAAAGCTGAAGTGTGACTGACATTTACCTGCTCAACCTGGCCATCTCT 341
QY 301 GATCTGCTTTTCTTATTACTCTCCATTTGGGCTCACTCTGCTGCAAAATGAGTGGTC 360
DB 342 GATCTGCTTTTCTTATTACTCTCCATTTGGGCTCACTCTGCTGCAAAATGAGTGGTC 401
QY 361 TTTGGGAATGCAATGTGCAAAATTTATTCACAGGCTGTATCACATCGGTATTTTGGCGA 420
DB 402 TTTGGGAATGCAATGTGCAAAATTTATTCACAGGCTGTATCACATCGGTATTTTGGCGA 461
QY 421 ATCTTCTTCATCATCTCTGCAATTCGATGATACCTGGCTATTGTCCATGCTGTGTT 480
DB 462 ATCTTCTTCATCATCTCTGCAATTCGATGATACCTGGCTATTGTCCATGCTGTGTT 521
QY 481 GCTTTAAAGCCAGGAGCGGTCACTTTGGGCTGTGCAAGTGTGATCACTGGTGGTG 540
DB 522 GCTTTAAAGCCAGGAGCGGTCACTTTGGGCTGTGCAAGTGTGATCACTGGTGGTG 581
QY 541 GCTGTGTTTCTGCTGTCAGAGGAATCATCTTTACTAAATGCCAGAAAGATCTCTT 600
DB 582 GCTGTGTTTCTGCTGTCAGAGGAATCATCTTTACTAAATGCCAGAAAGATCTCTT 641
QY 601 TATGTCTGTGGCCCTTATTTCCACGAGGATGGAATATTTCCACAAATAGGGAAC 660
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DB 642 TATGTCTGTGGCCCTTATTTTCCACGAGGATGGAATATTTCCACAAATAGGGAAC 701
QY 661 ATTTTGGGGCTGCTCTCGCGCTCATCATGCTGCTACTCGGGAAATCTGAAA 720
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DB 702 ATTTTGGGGCTGCTCTCGCGCTCATCATGCTGCTACTCGGGAAATCTGAAA 761
QY 721 ACCCTGCTTCGGTGTCTGAACAGAGAGGAGGATAGGGCAGTGAGTCACTTTCACC 780
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DB 762 ACCCTGCTTCGGTGTCTGAACAGAGAGGAGGATAGGGCAGTGAGTCACTTTCACC 821
QY 781 ATCATGATTGTTTACTTTCTTCTGACTCCCTATAACATTTGTCATCTCTCCCTGAACACC 840
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DB 822 ATCATGATTGTTTACTTTCTTCTGACTCCCTATAACATTTGTCATCTCTCCCTGAACACC 881
QY 841 TTCCAGGAATTTCTTGGCCTGAGTAACTGTGAAGCACCAGTCACTGATCCATCTATGCTTC 900
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DB 882 TTCCAGGAATTTCTTGGCCTGAGTAACTGTGAAGCACCAGTCACTGATCCATCTATGCTTC 941
QY 901 CAGGTGACAGACTCTTGGGATGACTCACTGCTGATCAATCCCATCTATGCTTC 960
DB 942 CAGGTGACAGACTCTTGGGATGACTCACTGCTGATCAATCCCATCTATGCTTC 1001
QY 961 GTTGGGAGAGTTCAGAG 980
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DB 1002 GTTGGGAGAGTTCAGAG 1021
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RESULT 5

US-08-446-669-3
Sequence 3, Application US/08446669
Patent No. 6132987
GENERAL INFORMATION:
APPLICANT: Charo, Israel
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,669
FILING DATE: May 25, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Neeley, Richard
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: UCAL-237/01US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5000
TELEFAX: 415-857-0663
TELEX: 380816CooLeypA
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1979 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 81..1160

US-08-446-669-3

Query Match 43.9%; Score 980; DB 3; Length 1979;
Best Local Similarity 100.0%; Pred. No. 2.3e-270;
Matches 980; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGATTGAACAAGGAGCGCATTTCCCGAGTACATCCACACATGCTGTCCACATCTCGTTCT 60
Db 42 GGATTGAACAAGGAGCGCATTTCCCGAGTACATCCACACATGCTGTCCACATCTCGTTCT 101

Qy 61 CGGTTTATCAGAAATACCAACAGAGCGGTGAAGAGTCAACACCTTTTTCATTATGAT 120
Db 102 CGGTTTATCAGAAATACCAACAGAGCGGTGAAGAGTCAACACCTTTTTCATTATGAT 161

Qy 121 TACGCTGCTCCCTGTCTATATAATTTGACGTGAAGCAAAATGGGGCCCAACTCTCGCTCG 180
Db 162 TACGCTGCTCCCTGTCTATATAATTTGACGTGAAGCAAAATGGGGCCCAACTCTCGCTCG 221

Qy 181 CTCTACTCGCTGCTGTCTATCTTTTGTGGGCAACATGCTGTCTCTCTCATCTTA 240
Db 222 CTCTACTCGCTGCTGTCTATCTTTTGTGGGCAACATGCTGTCTCTCTCATCTTA 281

Qy 241 ATAAACTGCAAAAAGCTGAAGTCTGTGACTGACATTTACTGCTCAACCTGGCCATCTCT 300
Db 282 ATAAACTGCAAAAAGCTGAAGTCTGTGACTGACATTTACTGCTCAACCTGGCCATCTCT 341

Qy 301 GATCTGCTTTTCTTATTACTCTCCCATTTGTGGGCTCACTCTCTGCTCAAAATGAGTGGTC 360
Db 342 GATCTGCTTTTCTTATTACTCTCCCATTTGTGGGCTCACTCTCTGCTCAAAATGAGTGGTC 401

Qy 361 TTGGGAATGCAATGCAATTTATTCACAGGCTGTATCACATCGSTTATTTTGGCGGA 420
Db 402 TTGGGAATGCAATGCAATTTATTCACAGGCTGTATCACATCGSTTATTTTGGCGGA 461

Qy 421 ATCTTCTTCATATCTCTCGTGAATCGATAGATACCTGTGCTATTTGCCATGCTGTTT 480
Db 462 ATCTTCTTCATATCTCTCGTGAATCGATAGATACCTGTGCTATTTGCCATGCTGTTT 521

Qy 481 GCTTTTAAAGCCAGGAGGTCACCTTTTGGGCTGTGACAGTGTGATCATCTGTTGGTG 540
Db 522 GCTTTTAAAGCCAGGAGGTCACCTTTTGGGCTGTGACAGTGTGATCATCTGTTGGTG 581

Qy 541 GCTGTGTTTCTGTGCTCCAGGAATCATCTTTACTTAAATGCCAGAAAGATTTCTGTT 600
Db 582 GCTGTGTTTCTGTGCTCCAGGAATCATCTTTACTTAAATGCCAGAAAGATTTCTGTT 641

Qy 601 TATGCTGTGGCCCTTATTTTCCAGGAGATGGAATTAATTTCCACAAATATGAGGAAC 660
Db 642 TATGCTGTGGCCCTTATTTTCCAGGAGATGGAATTAATTTCCACAAATATGAGGAAC 701

Qy 661 ATTTTGGGCTGCTGCTGCTGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db 702 ATTTTGGGCTGCTGCTGCTGCTGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 761

Qy 721 ACCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 762 ACCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 821

Qy 781 ATCATGATGTTTACTTCTTCTGGAATCCCTTATACATTTGATTCATCTCTGACAC 840
Db 822 ATCATGATGTTTACTTCTTCTGGAATCCCTTATACATTTGATTCATCTCTGACAC 881

Qy 841 TTCAGGAATTTCTGGGCTGAGTAACTGTGAAGGACCACTCACTGACCAAGCCACG 900
Db 882 TTCAGGAATTTCTGGGCTGAGTAACTGTGAAGGACCACTCACTGACCAAGCCACG 941

Qy 901 CAGGTGACAGACTCTTTGGGATGACTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db 942 CAGGTGACAGACTCTTTGGGATGACTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1001

Qy 961 GTTGGGGAAGTTCAGAG 980
Db 1002 GTTGGGGAAGTTCAGAG 1021

RESULT 6
PCT-US95-00476-3
Sequence 3, Application PC/TUS9500476
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins, Berliner & Carson
STREET: 201 N. Figueroa Street, 5th Floor
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90012-2628
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00476
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Berliner, Robert
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 5555-291
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-977-1001
TELEFAX: 310-977-1003
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1979 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 81..1160
PCT-US95-00476-3

Query Match 43.9%; Score 980; DB 5; Length 1979;
Best Local Similarity 100.0%; Pred. No. 2.3e-270;
Matches 980; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGATTGAACAAGGAGCGCATTTCCCGAGTACATCCACACATGCTGTCCACATCTCGTTCT 60
Db 42 GGATTGAACAAGGAGCGCATTTCCCGAGTACATCCACACATGCTGTCCACATCTCGTTCT 101

Qy 61 CGGTTTATCAGAAATACCAACAGAGCGGTGAAGAGTCAACACCTTTTTCATTATGAT 120
Db 102 CGGTTTATCAGAAATACCAACAGAGCGGTGAAGAGTCAACACCTTTTTCATTATGAT 161

Qy 121 TACGCTGCTCCCTGTCTATATAATTTGACGTGAAGCAAAATGGGGCCCAACTCTCGCTCG 180
Db 162 TACGCTGCTCCCTGTCTATATAATTTGACGTGAAGCAAAATGGGGCCCAACTCTCGCTCG 221

Qy 181 CTCTACTCGCTGCTGTCTATCTTTTGTGGGCAACATGCTGTCTCTCTCATCTTA 240
Db 222 CTCTACTCGCTGCTGTCTATCTTTTGTGGGCAACATGCTGTCTCTCTCATCTTA 281

Qy 241 ATAAACTGCAAAAAGCTGAAGTCTGTGACTGACATTTACTGCTCAACCTGGCCATCTCT 300
Db 282 ATAAACTGCAAAAAGCTGAAGTCTGTGACTGACATTTACTGCTCAACCTGGCCATCTCT 341

Qy 301 GATCTGCTTTTCTTATTACTCTCCCATTTGTGGGCTCACTCTCTGCTCAAAATGAGTGGTC 360

Db 342 GATCTGCTTTTCTTATATCTCTCCATTTGGGCTCACTCTGCTGCAAAATGAGTGGTTC 401
QY 361 TTTGGGAATCAATGTGCAAAATATTACAGGGCTGTATCATCATCGGTATTATTTGGCGGA 420
Db 402 TTTGGGAATCAATGTGCAAAATATTACAGGGCTGTATCATCATCGGTATTATTTGGCGGA 461
QY 421 ATCTTCTTCAATCCCTCTGACAAATGATAGATACCTGGCTATTGTCCATGCTGTGTT 480
Db 462 ATCTTCTTCAATCCCTCTGACAAATGATAGATACCTGGCTATTGTCCATGCTGTGTT 521
QY 481 GCTTTAAAGCCAGGAGGCTCACTTTGGGGTGTGACAAAGTGTGATCACTGGTGTGTT 540
Db 522 GCTTTAAAGCCAGGAGGCTCACTTTGGGGTGTGACAAAGTGTGATCACTGGTGTGTT 581
QY 541 GCTGTGTTGCTCTCTGCTCCAGGAATCATCTTTACTAAATGCCAGAAAGATATTCGTT 600
Db 582 GCTGTGTTGCTCTCTGCTCCAGGAATCATCTTTACTAAATGCCAGAAAGATATTCGTT 641
QY 601 TATGCTGTGGCCCTTATTTTCCACGAGGATGAATATTTCCACACAATATGAGAAC 660
Db 642 TATGCTGTGGCCCTTATTTTCCACGAGGATGAATATTTCCACACAATATGAGAAC 701
QY 661 ATTTGGGGCTGTCTGCTGCGCTGCTCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db 702 ATTTGGGGCTGTCTGCTGCGCTGCTCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 761
QY 721 ACCCTGCTTGGTGTGCAACGAGAGAGAGGATAGGAGGATAGGAGGATAGGAGGATAGG 780
Db 762 ACCCTGCTTGGTGTGCAACGAGAGAGAGGATAGGAGGATAGGAGGATAGGAGGATAGG 821
QY 781 ATCATGATTTTACTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Db 822 ATCATGATTTTACTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 881
QY 841 TTCAGGAATTTCTGGGCTGAGTAACTGTGAAGCACCAGTCAACTGGACCAAGCCACG 900
Db 882 TTCAGGAATTTCTGGGCTGAGTAACTGTGAAGCACCAGTCAACTGGACCAAGCCACG 941
QY 901 CAGGTGACAGACACTTTGGGATGACTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db 942 CAGGTGACAGACACTTTGGGATGACTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1001
QY 961 GTTGGGGAAGTTCAGAG 980
Db 1002 GTTGGGGAAGTTCAGAG 1021

RESULT 7

US-09-517-605-8

; Sequence 8, Application US/09517605

; Patent No. 6391567

; GENERAL INFORMATION:

; APPLICANT: Littman, Dan R.

; APPLICANT: Kwon, Douglas S.

; APPLICANT: van Kooyk, Yvette

; APPLICANT: Geijtenbeek, Tneo

; TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO

; FILE REFERENCE: 1049-1-017

; CURRENT APPLICATION NUMBER: US/09/517,605

; CURRENT FILING DATE: 2000-03-02

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 8

; LENGTH: 1059

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-517-605-8

Query Match

Best Local Similarity 28.5%; Score 635.6; DB 4; Length 1059;

Matches 738; Conservative 0; Mismatches 134; Indels 12; Gaps 1;

QY 110 TTGATTATGATTACGGTGTCCCTGCTCATATAAATTTGACGGAAGCAAAATTTGGGCCCAAC 169
Db 35 TCGATTATGATATACATGGAGCCCTGCAAAAAATCAATGTGAAGCAAAATCCAGCCGCC 94
QY 170 TCTGCTCCGCTACTACTCGCTGCTGTTTCACTTTGTTGTTTGGGGCAACATGCTGTCG 229
Db 95 TCTGCTCCGCTACTACTCGCTGCTGTTTCACTTTGTTTGGTTTGGGGCAACATGCTGTC 154
QY 230 TCTCATCTTAATAAAGCTGAAAGCTGAAAGCTGAAAGCTGAAAGCTGAAAGCTGAAAGCT 289
Db 155 TCTGCTGCTGATATAAAGCTGAAAGCTGAAAGCTGAAAGCTGAAAGCTGAAAGCTGAA 214
QY 290 TGGCCATCTCTGATGCTGCTTTTCTTATTAATCTCTCCATTTGTTGGGCTCACTCTGCT 349
Db 215 TGGCCATCTCTGATGCTGCTTTTCTTATTAATCTCTCCATTTGTTGGGCTCACTCTGCT 274
QY 350 ATGAGTGGGCTTTTGGGAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 409
Db 275 CCCAGTGGGCTTTTGGGAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 334
QY 410 ATTTGGGGGAATCTTCTTCAATCTCTCTGCAATGCAATGCAATGCAATGCAATGCAAT 469
Db 335 TCTTCTCTGGAATCTTCTTCAATCTCTCTGCAATGCAATGCAATGCAATGCAATGCAAT 394
QY 470 ATGCTGTGTTTCTTAAAGCCAGGAGGCTCACTTTGGGGTGTGACAAAGTGTGATCA 529
Db 395 ATGCTGTGTTTCTTAAAGCCAGGAGGCTCACTTTGGGGTGTGACAAAGTGTGATCA 454
QY 530 CCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 589
Db 455 CTTGGTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 514
QY 590 AAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 637
Db 515 AAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 574
QY 638 ATTTCCACACAATTAAGAGAAATTTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 697
Db 575 ATTTCCAGACATTAAGAGATGCTCATCTTGGGGCTGCTGCTGCTGCTGCTGCTGCTGCT 634
QY 698 TCTGCTACTCGGGAATCTGAAACCCCTGCTTGGGTGTCGAAACGAGAGAGAGCAT 757
Db 635 TCTGCTACTCGGGAATCTGAAACCCCTGCTTGGGTGTCGAAACGAGAGAGAGCAT 694
QY 758 GGGCAGTGAGAGTCACTTCAACCATGATTTTACTTCTTCTTCTTCTTCTTCTTCTTCT 817
Db 695 GGGCTGTGAGGCTTATCTTCAACCATGATTTTACTTCTTCTTCTTCTTCTTCTTCTTCT 754
QY 818 ACATTTGCTATCTCTGCAACACCTTCCAGGAATTTCTTGGGCTGAGTAACTGTTGAAAGCA 877
Db 755 ACATTTGCTATCTCTGCAACACCTTCCAGGAATTTCTTGGGCTGAGTAACTGTTGAAAGCA 814
QY 878 CCAGTCAACTGGACCAAGCCAGGAGTGTGACAGAGCTTTGGGATGACTCACTGCTGCA 937
Db 815 CTAACAGGTTGGACCAAGCCAGGAGTGTGACAGAGCTTTGGGATGACTCACTGCTGCA 874
QY 938 TCAATCCCATCATCTATGCTTCTTGGGGAAGTTCAGAGC 981
Db 875 TCAACCCCATCATCTATGCTTGTGGGGAAGTTCAGAGC 918

RESULT 8

US-08-724-984A-3

; Sequence 3, Application US/08724984A

; Patent No. 6388055

; GENERAL INFORMATION:

; APPLICANT: Derk Bergsma, Mary Brawner, and Usman Shabon

; TITLE OF INVENTION: No. 6388055el Mouse Genomic clone of the CC-

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SmithKline Beecham Corporation

Query Match

697 GGGTGGTGGCTGTGTTTGGGTCCTCT

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RESULT 10
US-09-087-232A-12
; Sequence 12, Application US/09087232A
; Patent No. 6153431
; GENERAL INFORMATION:
; APPLICANT: Quillent et al.
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
; TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
; NUMBER OF SEQUENCES: 23

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QY 593 ATTCCTGTTTANGTCTGTGGCCCTTATTTTCCA-----CGAGGATGGAATAATT 640
Db 757 GTCTTCATTACACCTGCAGCTCTCATTTTCCATACACAGTCAGTATCAATTCGGAAGAATT 816
QY 641 TCCACACAATAATGAGGAACATTTTGGGGCTGTCTCGCGCTGCTCATCATGTCATCT 700
Db 817 TCCAGACATTAAGATAGTCAATCTTGGGGCTGTCTCGCGCTGCTCATGTCATCT 876
QY 701 GCTACTCGGGAATCCCTGAAACCCCTGCTCGGTGTCGAAACGAGAAGAGGCATAGG 760
Db 877 GCTACTCGGGAATCCCTGAAACCCCTGCTCGGTGTCGAAACGAGAAGAGGCACAGG 936
QY 761 CAGTGAGAGTCATCTTCCACCATCATGATGTTTACCTTCTCTGTCGACCTCCCTATAACA 820
Db 937 CTGTGAGGCTTATCTTCCACCATCATGATGTTTATTTTCTCTGTCGGCTCCCTACACA 996
QY 821 TTGTGATCTCTCGAACACCTTCCAGGAATCTTCCGGCTGAGTAACTGTGAAAGCACCA 880
Db 997 TTGTGCTTCTCGAACACCTTCCAGGAATCTTCCGGCTGAGTAACTGTGAAAGTCA 1056
QY 881 GTCAACTGGACCAAGCCAGCTGACAGAGCTCTTGGGATGACTCATCTGTGTCATCA 940
Db 1057 ACAGTTGGACCAAGCTATGACAGTACAGAGACTCTTGGGATGACGCACTGTCTGCATCA 1116
QY 941 ATCCCATCATCTATGCTTCTGTTGGGAGAGTTTCAAGC 981
Db 1117 ACCCCATCATCTATGCTTCTGTCGGGAGAGTTTCAAGAAC 1157

RESULT 11

US-08-833-752-2
; Sequence 2, Application US/08833752
; Patent No. 6448375
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833.752
; FILING DATE: 9-APR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1477 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 240..1295
US-08-833-752-2

Query Match 28.3%; Score 632.6; DB 4; Length 1477;
Best Local Similarity 83.4%; Pred. No. 4.7e-171;
Matches 735; Conservative 0; Mismatches 134; Indels 12; Gaps 1;
QY 113 ATTATGATTACGGTGTCTCCCTGTGTCATAAAATTTGACGTGAAGCAAAATTTGGGGCCCACTCC 172
Db 277 ATTATTTATACATCGGAGCCCTGCGCAAAATCAATGTGAAGCAAAATGCGAGCGCCCTCC 336
QY 173 TGCCTCCGCTCTACTCCCTGCTGTTCATCTTTGCTTTTGTGGGCAACATGCTGTGTCGTC 232
Db 337 TGCCTCCGCTCTACTCCCTGCTGTTCATCTTTGCTTTTGTGGGCAACATGCTGTGTCATCC 396
QY 233 TCATCTTTAATAAAGCTGCAAAAGCTGAAGTCTTGTGACTGACATTTACCTGCTCAACCTGG 292
Db 397 TCATCTTGATTAAGCTGCAAAAGCTGAAGTCTTGTGACTGACATTTACCTGCTCAACCTGG 456
QY 293 CCATCTCTGATCTCTCTTTTCTTATTTACTCTCCCATTTGTGGGCTGACCTGCTGTCGCAATG 352
Db 457 CCATCTCTGATCTCTCTTTTCTTATTTACTGTCCTCTGCTGCTGCTGCTGCTGCTGCTGCT 516
QY 353 AGTGGGCTTTGGGAATGCAATGTCRAATTTATTCACAGGCTGTATCACATCGGTTATT 412
Db 517 AGTGGGCTTTGGGAATGCAATGTCRAATTTATTCACAGGCTGTATTTATGAGCTTCT 576
QY 413 TTGGCGGAATCTTCTTCATCATCTCTCTGACAAATCGATAGATACCTGCTATTTGTCATG 472
Db 577 TCTCTGGAATCTTCTTCATCATCTCTCTGACAAATCGATAGTACCTGCTGCTGCTGCTGCT 636
QY 473 CTGTGTTTGTCTTTAAAGCCAGGAGGTCACCTTTTGGGGTGGTGACAAAGTGTGATCACT 532
Db 637 CTGTGTTTGTCTTTAAAGCCAGGAGGTCACCTTTTGGGGTGGTGACAAAGTGTGATCACT 696
QY 533 GGTGGTGGCTGTGTTTCTGTCGCCAGGAATCATCTTTACTAAATGCCAAGAAAGAG 592
Db 697 GGGTGGTGGCTGTGTTTCTGTCGCCAGGAATCATCTTTACTAAATGCCAAGAAAGAG 756
QY 593 ATTCTGTTTATGCTGTGCTGCTTATTTTCCA-----CGAGGATGGAATAATT 640
Db 757 GTCITTCATTACACCTGTCAGCTCTCATTTTCCATACAGTCAGTATCAATTTCTGGAAGAATT 816
QY 641 TCCACACAATAATGAGGAACATTTTGGGGCTGTCTCGCGCTGCTCATCATGTCATCT 700
Db 817 TCCAGACATTAAGATAGTCAATCTTGGGGCTGTCTCGCGCTGCTCATGTCATCT 876
QY 701 GCTACTCGGGAATCCCTGAAACCCCTGCTCGGTGTCGAAACGAGAAGAGGCATAGG 760
Db 877 GCTACTCGGGAATCCCTGAAACCCCTGCTCGGTGTCGAAATGAGAAGAGAGGCACAGG 936
QY 761 CAGTGAGAGTCATCTTCCACCATCATGATGTTTACTTCTCTCTGCGACTCCCTATAACA 820
Db 937 CTGTGAGGCTTATCTTCCACCATCATGATGTTTATTTCTCTCTGCGCTCCCTACACA 996
QY 821 TTGTGATCTCTCTGACACCTTCCAGGAATTTCTCGGCTGAGTAACTGTGAAAGCACCA 880
Db 997 TTGTGCTTCTCTGACACCTTCCAGGAATTTCTTGGGCTGATATATTTGCTGATGCTCTA 1056
QY 881 GTCAACTGGACCAAGCCAGCTGACAGAGCTCTTGGGATGACTCATCTGTGTCATCA 940
Db 1057 ACAGTTGGACCAAGCTATGACAGTACAGAGACTCTTGGGATGACGCACTGTCTGCATCA 1116
QY 941 ATCCCATCATCTATGCTTCTGTTGGGAGAGTTTCAAGC 981
Db 1117 ACCCCATCATCTATGCTTCTGTCGGGAGAGTTTCAAGAAC 1157

RESULT 12
US-08-861-105-13
; Sequence 13, Application US/08861105
; Patent No. 6258527
; GENERAL INFORMATION:
; APPLICANT: LITTMAN, DAN R.
; APPLICANT: DENG, HONGKUI

Query Match	28.3%;	Score 632.6;	DB 4;	Length 3383;
Best Local Similarity	83.4%;	Pred. No. 7.3e-171;		
Matches 735;	Conservative 0;	Mismatches 134;	Indels 12;	Gaps 1;
113	ATTATGATTACGGTGCCTCCCTGTCATAAATTGACGTGAAGCAAAATGGGGCCCAACTCC	172		
92	ATTATTATACATCGGAGCCCTGCCAAAAATCAATGTGAAGCAAAATCGCAGCCCGCCTCC	151		
173	TGCCCTCCGCTCFACTCGCTGGTTCATCTTGGTTTTTGTGGCACACATGCTGGTGGTCC	232		
152	TGCCCTCCGCTCFACTCAGCTGGTGGTTCATCTTGGTTTTTGTGGCACACATGCTGGTCA	211		
233	TCATCTTAATAAACATGCAAAAAGCTGAAGTGGTGTGACTGACATTTTACCTGCTCAACCTGG	292		
212	TCATCCTGATAAACATGCAAAAAGCTGGAAGAGCATGACTGACATCTACCTGCTCAACCTGG	271		
293	CAATCTCGATCTGCTTTTTTCTTTTACTCTCCCATTTGTGGGCTCACTCTGTGCAGAAATG	352		
272	CAATCTCGAGCTGTTTTTCTCTTCTACTGTGCCCTTCTGGGCTCACTATGCTGGCGCCC	331		
353	AGTGGGCTCTTTGGGAATCGAATGTCAAAATATTACAGGGGCTGTATACATCGGTTATT	412		
332	AGTGGGACTTTTGGAAATACAAATGTCTCAACTCTTGACAGGGCTCTATTATTATAGGTTCT	391		

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; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3383 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 55..1110
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: /= "88C polynucleotide and amino acid
US-08-575-967A-1

Query Match 28.3%; Score 632.6; DB 4; Length 3383;
Best Local Similarity 83.4%; Pred. No. 7.3e-171;
Matches 735; Conservative 0; Mismatches 134; Indels 12; Gaps 1;

QY 113 ATTATGATTAGGTCCTCCCTGTCTATAAAATTGACGTGAAGCAAAATTGGGGCCCAACTCC 172
DB 92 ATTATTTATACATCGAGCCCTGCCAAAATCATGTGAGCAAAATCGACGCCGCTCC 151
QY 173 TGCCTCCGCTACTCGCTGTGTTCATCTTTGGTGGGCAACATGCTGTCGTC 232
DB 152 TGCCTCCGCTACTCGCTGTGTTCATCTTTGGTGGGCAACATGCTGTCATCC 211
QY 233 TCATCTTAATAAAGTGAAGAGCTGAAGTCTTGACTGACATTTACCTGCTCAACCTGG 292
DB 212 TCATCTGATAAATGCAAAAGCTGAGACATGACTGACATCTACCTGCTCAACCTGG 271
QY 293 CCATCTCTGARTCTCTTTCTTATTAATCTCCCATGTTGGGCTGCTGCTGCAATG 352
DB 272 CCATCTCTGACTGTTTTCTCTTACTGTCCTCCCTTCTGGGCTCACTATGCTCCGCC 331
QY 353 AGTGGCTCTTGGGAATCAATGTGCAAAATTAATACAGAGCTGTATCACATCGGTTAT 412
DB 332 AGTGGGACTTTGGAAATACAATGTGCAATCTTTCAGAGGCTCTATTTATAGCTTCT 391
QY 413 TTGGCGGAATCTTCTTCATCATCTCTCCGACAATCATGATACATGCTGCTATGTCATG 472
DB 392 TCTCTGGAATCTTCTTCATCATCTCTCCGACAATCATGATACATGCTGCTGTCATG 451
QY 473 CTGTGTTTGTCTTAAAGCCAGGAGCTCACTTTGGGCTGTCACAGTGTGATCACT 532
DB 452 CTGTGTTTGTCTTAAAGCCAGGAGCTCACTTTGGGCTGTCACAGTGTGATCACT 511
QY 533 GGTGCTGCTGTGTTGCTCTGCTCCAGGAATCATCTTTACTAAATGCCAAGAAAG 592
DB 512 GGTGCTGCTGTGTTGCTCTGCTCCAGGAATCATCTTTACCAGATCTCAAAAAGAG 571
QY 593 ATTCTGTTTATGCTGTGGCCCTTATTTCCA -----CGAGGATGGAATAAT 640
DB 572 GTCTTCATTACACCTGCACCTCTCAATTTCCATACAGTCAGATCAATTTCTGGAAGAT 631
QY 641 TCCACAATAATAGGAACAATTTGGGCTGGTCTCGCGCTGCTCATCATGGTCATCT 700
DB 632 TCCAGACATTAAGATAGTCACTTGGGCTGGTCTCGCGCTGCTTGTGTCATCT 691
QY 701 GCTACTCGGAATCTCGTAAACCCCTGCTCGGTGTCGAACAGAGAGAGCATAGGG 760
DB 692 GCTACTCGGAATCTCGTAAACCCCTGCTCGGTGTCGAACAGAGAGAGCATAGGG 751
QY 761 CAGTGAGATCATCTTCAACATCATGATTTTACTTTCTCTGACTCCCTATAACA 820
DB 752 CTGTGAGGCTTATCTTCAACATCATGATTTTACTTTCTCTGACTCCCTATAACA 811
QY 821 TTGTCATCTCTGAAACCTTCCAGGAATTTCTTGGGCTGAGTAACTGTGAAGACCA 880
DB 812 TTGTCCTCTCTGAAACCTTCCAGGAATTTCTTGGGCTGAAATAATTTGAGTAGCT 871
QY 881 GTCACCTGGACCAAGCCAGGTCACAGACTCTTGGGATGACTCTCACTGCTGATCA 940

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